

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/564,266

Source: IFWP

Date Processed by STIC: 2/7/07

# ENTERED



IFWP

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/564,266

DATE: 02/07/2007  
TIME: 10:03:55

Input Set : A:\40184-5.APP  
Output Set: N:\CRF4\02072007\J564266.raw

3 <110> APPLICANT: Yang, Hongyuan  
4 National University of Singapore  
6 <120> TITLE OF INVENTION: Triacylglycerol-Deficient Fission Yeast and Its Uses  
8 <130> FILE REFERENCE: 040184-000500US  
10 <140> CURRENT APPLICATION NUMBER: US 10/564,266  
11 <141> CURRENT FILING DATE: 2006-01-09  
13 <150> PRIOR APPLICATION NUMBER: US 60/485,385  
14 <151> PRIOR FILING DATE: 2003-07-09  
16 <150> PRIOR APPLICATION NUMBER: WO PCT/SG04/00205  
17 <151> PRIOR FILING DATE: 2004-07-09  
19 <160> NUMBER OF SEQ ID NOS: 24  
21 <170> SOFTWARE: PatentIn Ver. 2.1  
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26 <213> ORGANISM: Artificial Sequence  
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29 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR  
30 amplification primer PLH1-55  
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33 ggggtaccac accctatgg caaca 25  
36 <210> SEQ ID NO: 2  
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42 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR  
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45 <400> SEQUENCE: 2  
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49 <210> SEQ ID NO: 3  
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51 <212> TYPE: DNA  
52 <213> ORGANISM: Artificial Sequence  
54 <220> FEATURE:  
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59 cggatcccc acaaacaat atgataaa 28  
62 <210> SEQ ID NO: 4  
63 <211> LENGTH: 27  
64 <212> TYPE: DNA  
65 <213> ORGANISM: Artificial Sequence

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84 ggggtaccga atccatgggt agtgat                                26
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89 <212> TYPE: DNA
90 <213> ORGANISM: Artificial Sequence
92 <220> FEATURE:
93 <223> OTHER INFORMATION: Description of Artificial Sequence:primer DG11-53
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99 <210> SEQ ID NO: 7
100 <211> LENGTH: 27
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102 <213> ORGANISM: Artificial Sequence
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129 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR
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133 ataagaatgc ggccgcggaa gaactttgac acgtt                                35
136 <210> SEQ ID NO: 10
137 <211> LENGTH: 26
138 <212> TYPE: DNA

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159 ccatcgatgt agttccatca gatatt 26
162 <210> SEQ ID NO: 12
163 <211> LENGTH: 28
164 <212> TYPE: DNA
165 <213> ORGANISM: Artificial Sequence
167 <220> FEATURE:
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169   amplification primer pca23
171 <400> SEQUENCE: 12
172 ccgctcgagg gtaggttagta tagttaga 28
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176 <211> LENGTH: 19
177 <212> TYPE: DNA
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184 <400> SEQUENCE: 13
185 gagaaagaat gctgagtag 19
188 <210> SEQ ID NO: 14
189 <211> LENGTH: 18
190 <212> TYPE: DNA
191 <213> ORGANISM: Artificial Sequence
193 <220> FEATURE:
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195   primer in coding region of his3+
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198 gagtcattaa ttcattac 18
201 <210> SEQ ID NO: 15
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206 <220> FEATURE:
207 <223> OTHER INFORMATION: Description of Artificial Sequence:diagnostic PCR
208   primer in region outside of flanking fragment of
  
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209      dg1+
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225 <400> SEQUENCE: 16
226 gtatattagt attgcctaat
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243 <211> LENGTH: 30
244 <212> TYPE: DNA
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248 <223> OTHER INFORMATION: Description of Artificial Sequence:RT-PCR primer
249      PLH3
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256 <211> LENGTH: 29
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260 <220> FEATURE:
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268 <210> SEQ ID NO: 20
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271 <213> ORGANISM: Artificial Sequence
273 <220> FEATURE:
274 <223> OTHER INFORMATION: Description of Artificial Sequence:PCR
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277 <400> SEQUENCE: 20
278 tccccccgggt taggctgaca acttcaat

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281 <210> SEQ ID NO: 21  
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290 <400> SEQUENCE: 21  
291 ggaattccat atggccaata ataccactg 29  
294 <210> SEQ ID NO: 22  
295 <211> LENGTH: 28  
296 <212> TYPE: DNA  
297 <213> ORGANISM: Artificial Sequence  
299 <220> FEATURE:  
300 <223> OTHER INFORMATION: Description of Artificial Sequence:E. coli genomic  
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303 <400> SEQUENCE: 22 28  
304 tccccccgggt tatccaaaat gcgaccat  
307 <210> SEQ ID NO: 23  
308 <211> LENGTH: 345  
309 <212> TYPE: PRT  
310 <213> ORGANISM: Schizosaccharomyces pombe  
312 <220> FEATURE:  
313 <223> OTHER INFORMATION: diacylglycerol O-acyltransferase (dgal; GeneDB  
314 Accession No. SPCC1235.15)  
316 <400> SEQUENCE: 23  
317 Met Ser Glu Glu Thr Ser Ile Pro Gly Ile Ile Ala Ser Thr Pro Pro  
318 1 5 10 15  
320 Ile Ser Lys Asp Ser Arg Arg Asn Val Ser His Trp Leu Gln Ala Leu  
321 20 25 30  
323 Ala Val Phe Leu His Ser Val Ser Leu Thr Leu Thr Ala Ser Trp Tyr  
324 35 40 45  
326 Thr Val Leu Trp Ala Phe Leu Pro Phe Trp Pro Phe Leu Ile Val Tyr  
327 50 55 60  
329 Leu Ile Trp Leu Ile Tyr Asp Asp Gly Phe Val Thr Gly Lys Asp Arg  
330 65 70 75 80  
332 Gln Lys Arg Trp Leu Arg Asn Ala Pro Pro Tyr Arg Trp Phe Cys His  
333 85 90 95  
335 Tyr Phe Pro Ile Arg Leu His Lys Thr Thr Glu Leu Asp Ser Glu Lys  
336 100 105 110  
338 Asn Tyr Ile Phe Gly Tyr His Pro His Gly Ile Ile Ser Leu Gly Ala  
339 115 120 125  
341 Phe Gly Gly Phe Ala Ser Glu Gly Ala Asp Phe Ser Lys Leu Phe Pro  
342 130 135 140  
344 Gly Ile Asn Val Ser Val Leu Thr Leu Asn Ser Asn Phe Tyr Val Pro  
345 145 150 155 160  
347 Val Tyr Arg Asp Tyr Leu Met Ala Leu Asn Ile Asn Ser Val Ser Lys  
348 165 170 175  
350 Lys Ser Cys Val Ser Ile Leu Ser Arg Lys Pro Gly Asp Ser Val Leu

**VERIFICATION SUMMARY** DATE: 02/07/2007  
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